

SEQUENCE LISTING

<110> JCR Pharmaceuticals Co., Ltd.

<120> A nucleic acid molecule containing a gene encoding a fusion protein of an antibody and a physiologically active protein

<130> 1235JP

<150> JP2021-002567

<151> 2021-01-12

<160> 50

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an exemplified linker 1

<400> 1

Gly Gly Gly Gly Ser

1 5

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an exemplified linker 2

<400> 2

Gly Gly Gly Gly Gly Ser

1 5

<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of an exemplified linker 3

<400> 3

Ser Gly Gly Gly Gly

1 5

<210> 4

<211> 145

<212> DNA

<213> adeno-associated virus 2

<400> 4

ttggccactc cctctctgcg cgctcgctcg ctactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg 120

gccaaactcca tcactagggg ttcct 145

<210> 5

<211> 145

<212> DNA

<213> adeno-associated virus 2

<400> 5

aggaaccctt agtgatggag ttggccactc cctctctgcg cgctcgctcg ctactgagg 60

ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgag agagggagtg gccaa 145

<210> 6

<211> 141

<212> DNA

<213> Artificial Sequence

<220>

<223> A preferable example of nucleic acid sequence of the first
Inverted Terminal Repeat (first ITR) , synthetic sequence

<400> 6

cctgcaggca gctgcgcgct cgctcgctca ctgaggccgc ccgggcaaag cccgggcgtc 60

gggcgacctt tggtcgcccg gcctcagtga gcgagcgagc ggcgagagag ggagtggcca 120

actccatcac taggggttcc t 141

<210> 7

<211> 141

<212> DNA

<213> Artificial Sequence

<220>

<223> A preferable example of nucleic acid sequence of the second Inverted Terminal Repeat (second ITR) , synthetic sequence

<400> 7

aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctactgagg 60

ccgggcgacc aaaggtcgcc cgacgcccg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgag ctgcctgcag g 141

<210> 8

<211> 559

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of mouse alpha fetoprotein enhancer/mouse albumin promoter, synthetic sequence

<400> 8

agatcatttt gatggcagag ttcagtttac cgggtcacat tgtacctggg aagattcaag 60

gatttatgga aaaagtcaac aacaggagtc agagcagccg gaaaagcatg gactctgtac 120

ttaggactgc gctttgagca atggcacagc aagctataac cctgtttgca gtcagcacac 180

aaactgtggt tcaaagctcc actttatctc ttcttgtgga attcagatat cagatcagtt 240

ttgctcaaat gggagacaaa gagattaagc tcttatgtaa aatttgctgt ttacataac 300

tttaatgaat ggacaaagtc ttgtgcatgg ggggtgggggt ggggttagag gggaacagct 360

ccagatggca aacatacgca agggatttag tcaaacaact ttttggcaaa gatggtatga 420

ttttgtaatg gggtaggaac caatgaaatg cgaggtaagt atggttaata atctacagtt 480

attggttaaa gaagtatatt agagcgagtc tttctgcaca cagatcacct tcctatcaac 540

cccactagcc tctggcaaa 559

<210> 9
<211> 225
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of chicken beta actin/MVM chimeric intron,
synthetic sequence

<400> 9
ggagtcgctg cggtgccttc gccccgtgcc ccgctccgcg ccgcctcgcg ccgccccgcc 60
cggctctgac tgaccgcgtt actccacacag gtgagcgggc gggacggccc ttctcctccg 120
ggctgtaatt agcaagaggt aagggtttaa gggatgggtg gttggtgggg tattaatgtt 180
taattacctg gagcacctgc ctgaaatcac tttttttcag gttgg 225

<210> 10
<211> 593
<212> DNA
<213> Encephalomyocarditis virus

<400> 10
ccccccccc tctccctccc cccccctaa cggtactggc cgaagccgct tggaataagg 60
ccgggtgtgcg tttgtctata tggtattttc caccatattg ccgtcttttg gcaatgtgag 120
ggccccgaaa cctggccctg tcttcttgac gagcattcct aggggtcttt cccctctcgc 180
caaaggaatg caaggtctgt tgaatgtcgt gaaggaagca gttcctctgg aagcttcttg 240
aagacaaaca acgtctgtag cgaccctttg caggcagcgg aacccccac ctggcgacag 300
gtgcctctgc ggccaaaagc cacgtgtata agatacacct gcaaaggcgg cacaaccca 360
gtgccacgtt gtgagttgga tagttgtgga aagagtcaaa tggctctcct caagcgtatt 420
caacaagggg ctgaaggatg ccagaaggt accccattgt atgggatctg atctggggcc 480
tcggtgcaca tgctttacat gtgtttagtc gaggttaaaa aaacgtctag gcccccgaa 540
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<210> 11

<211> 760
<212> PRT
<213> Homo sapiens

<400> 11

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu
1 5 10 15

Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
20 25 30

Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
35 40 45

Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
50 55 60

Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
65 70 75 80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
85 90 95

Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro
100 105 110

Gly Glu Asp Phe Pro Ala Ala Arg Arg Leu Tyr Trp Asp Asp Leu Lys
115 120 125

Arg Lys Leu Ser Glu Lys Leu Asp Ser Thr Asp Phe Thr Gly Thr Ile
130 135 140

Lys Leu Leu Asn Glu Asn Ser Tyr Val Pro Arg Glu Ala Gly Ser Gln
145 150 155 160

Lys Asp Glu Asn Leu Ala Leu Tyr Val Glu Asn Gln Phe Arg Glu Phe
165 170 175

Lys Leu Ser Lys Val Trp Arg Asp Gln His Phe Val Lys Ile Gln Val
180 185 190

Lys Asp Ser Ala Gln Asn Ser Val Ile Ile Val Asp Lys Asn Gly Arg
195 200 205

Leu Val Tyr Leu Val Glu Asn Pro Gly Gly Tyr Val Ala Tyr Ser Lys
210 215 220

Ala Ala Thr Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys
225 230 235 240

Lys Asp Phe Glu Asp Leu Tyr Thr Pro Val Asn Gly Ser Ile Val Ile
245 250 255

Val Arg Ala Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu
260 265 270

Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe
275 280 285

Pro Ile Val Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly
290 295 300

Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln
305 310 315 320

Phe Pro Pro Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr
325 330 335

Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp
340 345 350

Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser
355 360 365

Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Ile
370 375 380

Lys Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Phe Val Glu Pro Asp
385 390 395 400

His Tyr Val Val Val Gly Ala Gln Arg Asp Ala Trp Gly Pro Gly Ala
405 410 415

Ala Lys Ser Gly Val Gly Thr Ala Leu Leu Leu Lys Leu Ala Gln Met
420 425 430

Phe Ser Asp Met Val Leu Lys Asp Gly Phe Gln Pro Ser Arg Ser Ile
435 440 445

Ile Phe Ala Ser Trp Ser Ala Gly Asp Phe Gly Ser Val Gly Ala Thr
450 455 460

Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys Ala Phe Thr
465 470 475 480

Tyr Ile Asn Leu Asp Lys Ala Val Leu Gly Thr Ser Asn Phe Lys Val
485 490 495

Ser Ala Ser Pro Leu Leu Tyr Thr Leu Ile Glu Lys Thr Met Gln Asn
500 505 510

Val Lys His Pro Val Thr Gly Gln Phe Leu Tyr Gln Asp Ser Asn Trp
515 520 525

Ala Ser Lys Val Glu Lys Leu Thr Leu Asp Asn Ala Ala Phe Pro Phe
530 535 540

Leu Ala Tyr Ser Gly Ile Pro Ala Val Ser Phe Cys Phe Cys Glu Asp
545 550 555 560

Thr Asp Tyr Pro Tyr Leu Gly Thr Thr Met Asp Thr Tyr Lys Glu Leu

565

570

575

Ile Glu Arg Ile Pro Glu Leu Asn Lys Val Ala Arg Ala Ala Ala Glu
 580 585 590

Val Ala Gly Gln Phe Val Ile Lys Leu Thr His Asp Val Glu Leu Asn
 595 600 605

Leu Asp Tyr Glu Arg Tyr Asn Ser Gln Leu Leu Ser Phe Val Arg Asp
 610 615 620

Leu Asn Gln Tyr Arg Ala Asp Ile Lys Glu Met Gly Leu Ser Leu Gln
 625 630 635 640

Trp Leu Tyr Ser Ala Arg Gly Asp Phe Phe Arg Ala Thr Ser Arg Leu
 645 650 655

Thr Thr Asp Phe Gly Asn Ala Glu Lys Thr Asp Arg Phe Val Met Lys
 660 665 670

Lys Leu Asn Asp Arg Val Met Arg Val Glu Tyr His Phe Leu Ser Pro
 675 680 685

Tyr Val Ser Pro Lys Glu Ser Pro Phe Arg His Val Phe Trp Gly Ser
 690 695 700

Gly Ser His Thr Leu Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys
 705 710 715 720

Gln Asn Asn Gly Ala Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala
 725 730 735

Leu Ala Thr Trp Thr Ile Gln Gly Ala Ala Asn Ala Leu Ser Gly Asp
 740 745 750

Val Trp Asp Ile Asp Asn Glu Phe
 755 760

<210> 12
<211> 226
<212> PRT
<213> Artificial Sequence

<220>
<223> An example of amino acid sequence of Fab region of the heavy chain of anti-hTfR antibody

<400> 12

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 210 215 220

His Thr
 225

<210> 13
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence of an exemplified linker 4

<400> 13

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 14
 <211> 525
 <212> PRT
 <213> Homo sapiens

<400> 14

Ser Glu Thr Gln Ala Asn Ser Thr Thr Asp Ala Leu Asn Val Leu Leu
 1 5 10 15

Ile Ile Val Asp Asp Leu Arg Pro Ser Leu Gly Cys Tyr Gly Asp Lys
20 25 30

Leu Val Arg Ser Pro Asn Ile Asp Gln Leu Ala Ser His Ser Leu Leu
35 40 45

Phe Gln Asn Ala Phe Ala Gln Gln Ala Val Cys Ala Pro Ser Arg Val
50 55 60

Ser Phe Leu Thr Gly Arg Arg Pro Asp Thr Thr Arg Leu Tyr Asp Phe
65 70 75 80

Asn Ser Tyr Trp Arg Val His Ala Gly Asn Phe Ser Thr Ile Pro Gln
85 90 95

Tyr Phe Lys Glu Asn Gly Tyr Val Thr Met Ser Val Gly Lys Val Phe
100 105 110

His Pro Gly Ile Ser Ser Asn His Thr Asp Asp Ser Pro Tyr Ser Trp
115 120 125

Ser Phe Pro Pro Tyr His Pro Ser Ser Glu Lys Tyr Glu Asn Thr Lys
130 135 140

Thr Cys Arg Gly Pro Asp Gly Glu Leu His Ala Asn Leu Leu Cys Pro
145 150 155 160

Val Asp Val Leu Asp Val Pro Glu Gly Thr Leu Pro Asp Lys Gln Ser
165 170 175

Thr Glu Gln Ala Ile Gln Leu Leu Glu Lys Met Lys Thr Ser Ala Ser
180 185 190

Pro Phe Phe Leu Ala Val Gly Tyr His Lys Pro His Ile Pro Phe Arg
195 200 205

Tyr Pro Lys Glu Phe Gln Lys Leu Tyr Pro Leu Glu Asn Ile Thr Leu

210

215

220

Ala Pro Asp Pro Glu Val Pro Asp Gly Leu Pro Pro Val Ala Tyr Asn
 225 230 235 240

Pro Trp Met Asp Ile Arg Gln Arg Glu Asp Val Gln Ala Leu Asn Ile
 245 250 255

Ser Val Pro Tyr Gly Pro Ile Pro Val Asp Phe Gln Arg Lys Ile Arg
 260 265 270

Gln Ser Tyr Phe Ala Ser Val Ser Tyr Leu Asp Thr Gln Val Gly Arg
 275 280 285

Leu Leu Ser Ala Leu Asp Asp Leu Gln Leu Ala Asn Ser Thr Ile Ile
 290 295 300

Ala Phe Thr Ser Asp His Gly Trp Ala Leu Gly Glu His Gly Glu Trp
 305 310 315 320

Ala Lys Tyr Ser Asn Phe Asp Val Ala Thr His Val Pro Leu Ile Phe
 325 330 335

Tyr Val Pro Gly Arg Thr Ala Ser Leu Pro Glu Ala Gly Glu Lys Leu
 340 345 350

Phe Pro Tyr Leu Asp Pro Phe Asp Ser Ala Ser Gln Leu Met Glu Pro
 355 360 365

Gly Arg Gln Ser Met Asp Leu Val Glu Leu Val Ser Leu Phe Pro Thr
 370 375 380

Leu Ala Gly Leu Ala Gly Leu Gln Val Pro Pro Arg Cys Pro Val Pro
 385 390 395 400

Ser Phe His Val Glu Leu Cys Arg Glu Gly Lys Asn Leu Leu Lys His
 405 410 415

Phe Arg Phe Arg Asp Leu Glu Glu Asp Pro Tyr Leu Pro Gly Asn Pro
420 425 430

Arg Glu Leu Ile Ala Tyr Ser Gln Tyr Pro Arg Pro Ser Asp Ile Pro
435 440 445

Gln Trp Asn Ser Asp Lys Pro Ser Leu Lys Asp Ile Lys Ile Met Gly
450 455 460

Tyr Ser Ile Arg Thr Ile Asp Tyr Arg Tyr Thr Val Trp Val Gly Phe
465 470 475 480

Asn Pro Asp Glu Phe Leu Ala Asn Phe Ser Asp Ile His Ala Gly Glu
485 490 495

Leu Tyr Phe Val Asp Ser Asp Pro Leu Gln Asp His Asn Met Tyr Asn
500 505 510

Asp Ser Gln Gly Gly Asp Leu Phe Gln Leu Leu Met Pro
515 520 525

<210> 15

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> An example of amino acid sequence of the light chain of anti-hTfR
antibody

<400> 15

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 16

<211> 226
<212> PRT
<213> Artificial Sequence

<220>

<223> An example of amino acid sequence of the heavy chain of anti-hTfR antibody

<400> 16

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr
225

<210> 17
<211> 208
<212> DNA
<213> Bos taurus

<400> 17
ctgtgccttc tagttgccag ccatctgttg ttgcccctc ccccgtcct tccttgaccc 60
tggaagggtg cactcccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc 120
tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag ggggaggatt 180
gggaagacaa tagcaggcat gctgggga 208

<210> 18
<211> 4744
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of the DNA fragment synthesized for
construction of pAAV-mMAP-Fab-hI2S vector, synthetic sequence

<400> 18
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ctgggaagat tcaaggattt atggaaaaag tcaacaacag gagtcagagc agccggaaaa 120

gcatggactc tgtacttagg actgcgcttt gagcaatggc acagcaagct ataaccctgt	180
ttgcagtcag cacacaaact gtggttcaaa gctccacttt atctcttctt gtggaattca	240
gatatcagat cagttttgct caaatgggag acaaagagat taagctctta tgtaaaattt	300
gctgttttac ataactttaa tgaatggaca aagtcttgtg catgggggtg ggggtggggt	360
tagaggggaa cagctccaga tggcaaacat acgcaaggga tttagtcaaa caactttttg	420
gcaaagatgg tatgattttg taatggggta ggaaccaatg aaatgcgagg taagtatggt	480
taataatcta cagttattgg ttaaagaagt atattagagc gagtctttct gcacacagat	540
caccttccta tcaacccac tagcctctgg caaaggtagc agtgtacagg gagtcgctgc	600
gttgcccttcg ccccggtgccc cgctccgcgc cgctccgcgc cgcccgcccc ggctctgact	660
gaccgcgtta ctcccacagg tgagcgggcg ggacggccct tctcctccgg gctgtaatta	720
gcaagaggta agggtttaag ggatggttgg ttggtggggt attaatgttt aattacctgg	780
agcacctgcc tgaaatcact ttttttcagg ttggacgcgt cgccaccatg ggttggagcc	840
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agtctggagc agagggtgaaa aagcccgggg agtctctgaa gatttcctgt aagggttctg	960
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agtggatggg ggacatctac cccggcggag actaccctac atacagcgag aagttcaagg	1080
tccaggtcac catctcagcc gacaagtcca tcagcaccgc ctacctgcag ttgagcagcc	1140
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cctactgggg ccaaggaacc ctggtcaccg tctcctcagc tagcaccaag ggcccatcgg	1260
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tggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc gccctgacca	1380
gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc ctcagcagcg	1440
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agcccagcaa caccaagggtg gacaagaaag ttgagccgaa gagctgtgat aagacgcata	1560

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attccatacg caccatagac tatagggtata ctgtgtgggt tggcttcaat cctgatgaat	3060

ttctagctaa cttttctgac atccatgcag gggaactgta ttttgtggat tctgacccat	3120
tgcaggatca caatatgtat aatgattccc aagggtggaga ctttttccag ttgttgatgc	3180
cttaataagc ggccgcccc cccccctctc cctccccccc ccctaacgtt actggccgaa	3240
gccgcttgga ataaggccgg tgtgcgtttg tctatatgtt attttccacc atattgccgt	3300
cttttggcaa tgtgagggcc cggaacctg gccctgtctt cttgacgagc attcctaggg	3360
gtctttcccc tctcgccaaa ggaatgcaag gtctgttgaa tgtcgtgaag gaagcagttc	3420
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tctcctcaag cgtattcaac aaggggctga aggatgcccc gaaggtaccc cattgtatgg	3660
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gccacaacca tgggctggag ctggattctg ctgttcctcc tgagcgtgac agcaggagtg	3840
cacagcgaca tcgtgatgac ccagactccc ctgagcctga gcgtgacacc tggccagcct	3900
gccagcatca gctgcagaag ctctcagagc ctggtgcaca gcaacggcaa cacctacctg	3960
cactggatatc tgcagaagcc cggccagagc cctcagctgc tgatctacaa ggtgtccaac	4020
agattcagcg gcgtgcccga cagattctcc ggcagcggct ctggcaccga cttcacctg	4080
aagatttcca gagtgggaagc cgaggacgtg ggcgtgtact actgcagcca gagcaccac	4140
gtgccctgga cattcggcca gggcaccaag gtggaaatca agagaaccgt ggccgctccc	4200
agcgtgttca tcttcccacc tagcgacgag cagctgaagt ccggcacagc ctctgtcgtg	4260
tgcttgctga acaacttcta cccccgcgag gccaaaggtgc agtggaaagg ggacaacgcc	4320
ctgcagagcg gcaacagcca ggaaagcgtg accgagcagg actccaagga cagcacctac	4380
agcctgagca gcacctgac cctgagcaag gccgactacg agaagcaciaa ggtgtacgcc	4440
tgcgaagtga cccaccaggg cctgtctagc cccgtgacca agagcttcaa cagaggcgag	4500

tgctaaat	ttt aaatgcggcc gcattt	aaat ctgtgccttc tagttgccag ccatctgttg	4560
tttgc	ccctc ccccg	tgccct tccttgaccc tggaagg	4620
tgccact	gtcctttcct		
aataaa	atga ggaaattgca tcgcattgtc	tgagtaggtg tcattctatt ctgggggggtg	4680
gggtgggg	ca ggacagcaag ggggaggatt	gggaagacaa tagcaggcat gctgggggaag	4740
atct			4744

<210> 19
 <211> 2820
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of the DNA fragment synthesized for construction of pR2(mod)C6 vector, synthetic sequence

<400> 19		
agcgctc	ggga ccgggcgcgc tcactggccg tcgttttaca acgtcgtgac tgggaaaacc	60
ctgtacaggc	tgaccgggtgt tgcctaggtg aatggcgaat ggtcagggtg cacttttcgg	120
ggaaatgtgc	gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg	180
ctcatgagac	aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt	240
attcaacatt	tccgtgtcgc ctttattccc ttttttgcgg catTTTgcct tcctgttttt	300
gctcacc	cag aaacgctggg gaaagtaaaa gatgctgaag atcagttggg tgcacgagt	360
ggttacatcg	aactggatct caacagcggg aagatccttg agagttttcg ccccgaagaa	420
cgTTTTccaa	tgatgagcac ttttaaagtt ctgctatgtg gcgcgggtatt atcccgtatt	480
gacgccgggc	aagagcaact cggtcgccgc atacactatt ctcagaatga cttggttgag	540
tactcaccag	tcacagaaaa gcatcttacg gatggcatga cagtaagaga attatgcagt	600
gctgccataa	ccatgagtga taacactgcg gccaaacttac ttctgacaac gatcggagga	660
ccgaaggagc	taaccgcttt tttgcacaac atgggggatc atgtaactcg ctttgatcgt	720
tgggaaccgg	agctgaatga agccatacca aacgacgagc gtgacaccac gatgcctgta	780
gcaatggcaa	caacgttgcg caaactatta actggcgaac tacttactct agcttcccgg	840

caacaattaa tagactggat ggaggcggat aaagttgcag gaccacttct gcgctcggcc	900
cttccggctg gctggtttat tgctgataaa tctggagccg gtgagcgtgg gtctcgcggt	960
atcattgcag cactggggcc agatggtaag ccctcccgtat tcgtagttat ctacacgacg	1020
gggagtcagg caactatgga tgaacgaaat agacagatcg ctgagatagg tgcctcactg	1080
attaagcatt ggtaactgtc agaccaagtt tactcatata tacttttagat tgatttaaaa	1140
cttcattttt aatttaaaaag gatctaggtg aagatccttt ttgataatct catgacccaa	1200
atcccttaac gtgagttttc gttccactga gcgtcagacc ccgtagaaaa gatcaaagga	1260
tcttcttgag atcctttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg	1320
ctaccagcgg tggtttggtt gccggatcaa gagctaccaa ctctttttcc gaaggtaact	1380
ggcttcagca gagcgcagat accaaatact gttcttctag tgtagccgta gttaggccac	1440
cacttcaaga actctgtagc accgcctaca tacctcgctc tgctaatacct gttaccagtg	1500
gctgctgcca gtggcgataa gtcgtgtctt accgggttgg actcaagacg atagttaccg	1560
gataaggcgc agcggtcggg ctgaacgggg gggtcgtgca cacagcccag cttggagcga	1620
acgacctaca ccgaactgag atacctacag cgtgagctat gagaaagcgc cacgcttccc	1680
gaaggggagaa aggcggacag gtatccggta agcggcaggg tcggaacagg agagcgcacg	1740
agggagcttc caggggggaaa cgcctggtat ctttatagtc ctgtcgggtt tcgccacctc	1800
tgacttgagc gtcgattttt gtgatgctcg tcaggggggc ggagcctatg gaaaaacgcc	1860
agcaacgcgg cttttttacg gttcctggcc ttttgctggc cttttgctca catgttcttt	1920
cctgcgttat cccctgattc tgtggataac cgtattaccg cttttgagtg agctgatacc	1980
gctcgccgca gccgaacgac cgagcgcagc gagtcagtga gcgaggaaagc ggaagagcgc	2040
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aggtttcccg actggaaagc gggcagtgag cgcaacgcaa ttaatgtgag ttagctcact	2160
cattaggcac ccaggcttt acactttatg cttccggctc gtatgttggtg tggaattgtg	2220
agcggataac aatttcacac aggaaacagc tatgaccatg attacgcaa cggaccggga	2280
gggggtggagt cgtgacgtga attacgtcat aggggttaggg aggtcctgta ttagagggtca	2340

cgtgagtgtt ttgcgacatt ttgcgacacc atgtggtctc gctggggggg ggggcccag	2400
tgagcacgca gggctctccat tttgaagcgg gaggtttgaa cgcgagccg ccacgccggg	2460
gttttacgag attgtgatta aggtccccag cgaccttgac gagcatctgc ccggcatttc	2520
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ggatctgaat ctgattgagc aggcacccct gaccgtggcc gagaagctgc agcgcgactt	2640
tctgacggaa tggcgccgtg tgagtaaggc cccggaggcc cttttctttg tgcaatttga	2700
gaaggagag agctacttcc acatgcacgt gctcgtggaa accaccgggg tgaaatccat	2760
ggttttggga cgtttcctga gtcagattcg cgaaaaactg attcagagaa tttaccgcgg	2820

<210> 20
 <211> 2911
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of the DNA fragment synthesized for construction of pR2(mod)C8 vector, synthetic sequence

<400> 20	
aagcttcgat caactacgca gacaggtacc aaaacaaatg ttctcgtcac gtgggcatga	60
atctgatgct gtttccctgc agacaatgcg agagaatgaa tcagaattca aatatctgct	120
tcactcacgg acagaaagac tgtttagagt gctttcccgt gtcagaatct caaccgttt	180
ctgtcgtcaa aaaggcgtat cagaaactgt gctacattca tcatatcatg ggaaagggtgc	240
cagacgcttg cactgcctgc gatctgggtca atgtggattt ggatgactgc atctttgaac	300
aataaatgat ttaaatcagg tatggctgcc gatggttatc ttccagattg gctcgaggac	360
aacctctctg agggcattcg cgagtgggtg gacttgaaac ctggagcccc gaaacccaaa	420
gccaaccagc aaaagcagga cgacggccgg ggtctggtgc ttcctggcta cagtacctc	480
ggacccttca acggactcga caagggggag cccgtcaacg cggcggatgc agcggccctc	540
gagcacgaca aggcctacga ccagcagctc aaagcgggtg acaatccgta cctgcggtat	600
aaccacgccg acgccgagtt tcaggagcgt ctgcaagaag atacgtcttt tgggggcaac	660

ctcgggcgag cagtcttcca ggccaagaag agggttctcg aaccttttgg tctggttgag	720
gaaggtgcta agacggctcc tggaaagaaa cgtccggtag agcagtcgcc acaagagcca	780
gactcctcct cgggcattgg caagacaggc cagcagcccc ctaaaaagag actcaatttt	840
ggtcagactg gcgactcaga gtcagtcccc gaccacacaac ctctcggaga acctccagca	900
acccccgctg ctgtgggacc tactacaatg gcttcaggcg gtggcgcacc aatggcagac	960
aataacgaag gcgccgacgg agtgggtaat gcctcaggaa attggcattg cgattccaca	1020
tggctgggcg acagagtcac caccaccagc acccgaacat gggccttgcc cacctataac	1080
aaccacctct acaagcaaat ctccagtgtc tcaacggggg ccagcaacga caaccactac	1140
ttcggctaca gcacccccctg ggggtatttt gatttcaaca gattccactg ccattttctca	1200
ccacgtgact ggcagcgact catcaacaac aattggggat tccggcccaa gagactcaac	1260
ttcaagctct tcaacatcca agtcaaggag gtcacgacga atgatggcgt cacgaccatc	1320
gctaataacc ttaccagcac ggttcaagtc ttctcggact cggagtacca gttgccgtac	1380
gtcctcggct ctgcgcacca gggctgcctc cctccgttcc cggcggacgt gttcatgatt	1440
ccgcagtagc gctacctaac gctcaacaat ggcagccagg cagtgggacg gtcacccctt	1500
tactgcctgg aatattttcc atcgcagatg ctgagaacgg gcaataactt taccttcagc	1560
tacaccttcg aggacgtgcc tttccacagc agctacgcgc acagccagag cctggaccgg	1620
ctgatgaatc ctctcatcga ccagtacctg tattacctga acagaactca gaatcagtcc	1680
ggaagtgccc aaaacaagga cttgctgttt agccgggggt ctccagctgg catgtctgtt	1740
cagcccaaaa actggctacc tggaccctgt taccggcagc agcgcgtttc taaaacaaaa	1800
acagacaaca acaacagcaa ctttacctgg actggtgctt caaaatataa ccttaatggg	1860
cgtgaatcta taatcaaccc tggcactgct atggcctcac acaaagacga caaagacaag	1920
ttctttccca tgagcgggtg catgatTTTT ggaaaggaga gcgccggagc ttcaaact	1980
gcattggaca atgtcatgat cacagacgaa gaggaaatca aagccactaa ccccggtggc	2040
accgaaagat ttgggactgt ggcagtcaat ctccagagca gcagcacaga ccctgcgacc	2100

ggagatgtgc atgttatggg agccttacct ggaatggtgt ggcaagacag agacgtatac	2160
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ctcatgggcg gctttggact taagcaccgc cctcctcaga tcctcatcaa aaacacgcct	2280
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tattccacag gacaagtgag cgtggagatt gaatgggagc tgcagaaaga aaacagcaaa	2400
cgctggaatc ccgaagtgca gtatacatct aactatgcaa aatctgcaa cgttgatttc	2460
actgtggaca acaatggact ttatactgag cctcgcccca ttggcaccgc ttacctcacc	2520
cgtcccctgt aattgcttgt taatcaataa accgtttaat tcgtttcagt tgaactttgg	2580
tctctgcgta tttctttctt atctagtttc catggctacg tagataagta gcatggcggg	2640
ttaatcatta actacagccc gggcgtttaa acagcgggcg gaggggtgga gtcgtgacgt	2700
gaattacgtc ataggggttag ggaggtcctg tattagaggt cacgtgagtg ttttgcgaca	2760
ttttgcgaca ccatgtggtc tcgctggggg ggggggcccc agtgagcacg cagggtctcc	2820
attttgaagc gggaggtttg aacgagcgct cggaccgggc gcgctcactg gccgtcgttt	2880
tacaacgtcg tgactgggaa aaccctgtac a	2911

<210> 21
 <211> 2038
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of Rep region of serotype 2 AAV containing
 p5 promoter, synthetic sequence

<400> 21	
ggaggggtgg agtcgtgacg tgaattacgt catagggtta gggaggtcct gtattagagg	60
tcacgtgagt gttttgcgac attttgcgac accatgtggt ctcgctgggg gggggggccc	120
gagtgagcac gcagggtctc cattttgaag cgggaggttt gaacgcgcag ccgccacgcc	180
ggggttttac gagattgtga ttaaggtccc cagcgacctt gacgagcatc tgcccggcat	240
ttctgacagc tttgtgaact ggggtggccga gaaggaatgg gagttgccgc cagattctga	300

catggatctg aatctgattg agcaggcacc cctgaccgtg gccgagaagc tgcagcgcga	360
ctttctgacg gaatggcgcc gtgtgagtaa ggccccggag gcccttttct ttgtgcaatt	420
tgagaaggga gagagctact tccacatgca cgtgctcgtg gaaaccaccg ggggtgaaatc	480
catggttttg ggacgtttcc tgagtcagat tcgcgaaaaa ctgattcaga gaattttaccg	540
cgggatcgag ccgactttgc caaactgggt cgcggtcaca aagaccagaa atggcgccgg	600
aggcggggaac aaggtgggtg atgagtgcta catccccaat tacttgctcc ccaaaaccca	660
gcctgagctc cagtgggcgt ggactaatat ggaacagtat ttaagcgctt gtttgaatct	720
cacggagcgt aaacggttgg tggcgagca tctgacgcac gtgtcgcaga cgcaggagca	780
gaacaaagag aatcagaatc ccaattctga tgcgccggtg atcagatcaa aaacttcagc	840
caggtacatg gagctggctg ggtggctcgt ggacaagggg attacctcgg agaagcagtg	900
gatccaggag gaccaggcct catacatctc cttcaatgcg gcctccaact cgcggtccca	960
aatcaaggct gccttggaaca atgcgggaaa gattatgagc ctgactaaaa ccgccccga	1020
ctacctggtg ggccagcagc ccgtggagga catttccagc aatcggattt ataaaaat	1080
ggaactaaac ggggtacgat cccaatatgc ggcttccgtc tttctgggat gggccacgaa	1140
aaagttcggc aagaggaaca ccatctggct gtttgggcct gcaactaccg ggaagaccaa	1200
catcgcgag gccatagccc aactgtgcc cttctacggg tgcgtaaact ggaccaatga	1260
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gaccgccaag gtcgtggagt cggccaaagc cattctcgga ggaagcaagg tgcgcgtgga	1380
ccagaaatgc aagtcctcgg ccagataga ccgactccc gtgatcgtca cctccaacac	1440
caacatgtgc gccgtgattg acgggaactc aacgacctt gaacaccagc agccgttgca	1500
agaccggatg ttcaaatttg aactaccccg ccgtctggat catgactttg ggaaggtcac	1560
caagcaggaa gtcaaagact ttttccggtg ggcaaaggat cacgtggttg aggtggagca	1620
tgaattctac gtcaaaaagg gtggagccaa gaaaagaccc gccccagtg acgcagatat	1680
aagtgagccc aaacgggtgc gcgagtcagt tgcgcagcca tcgacgtcag acgcggaagc	1740
ttcgatcaac tacgcagaca ggtacaaaaa caaatgttct cgtcacgtgg gcatgaatct	1800

gatgctgttt ccctgcagac aatgcgagag aatgaatcag aattcaaata tctgcttcac	1860
tcacggacag aaagactgtt tagagtgtt tcccgtgtca gaatctcaac ccgtttctgt	1920
cgtcaaaaag gcgtatcaga aactgtgcta cattcatcat atcatgggaa aggtgccaga	1980
cgcttgcaact gcctgcgatc tggatcaatgt ggatttggat gactgcatct ttgaacaa	2038

<210> 22
 <211> 2214
 <212> DNA
 <213> adeno-associated virus 8

<400> 22	
atggctgccg atggttatct tccagattgg ctcgaggaca acctctctga gggcattcgc	60
gagtgggtggg cgctgaaacc tggagccccg aagcccaaag ccaaccagca aaagcaggac	120
gacggccggg gtctggtgct tcctggctac aagtacctcg gacccttcaa cggactcgac	180
aaggggggagc ccgtcaacgc ggcggacgca gcggccctcg agcacgacaa ggcctacgac	240
cagcagctgc aggcgggtga caatccgtac ctgcggtata accacgccga cgccgagttt	300
caggagcgtc tgcaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaagaagc gggttctcga acctctcggc ctggttgagg aaggcgctaa gacggctcct	420
ggaaaagaaga gaccggtaga gccatcacc cagcgttctc cagactcctc tacgggcatc	480
ggcaagaaaag gccaacagcc cgccagaaaa agactcaatt ttggtcagac tggcgactca	540
gagtcagttc cagaccctca acctctcgga gaacctccag cagcgccctc tgggtgtggga	600
cctaatacaa tggctgcagg cgggtggcgca ccaatggcag acaataacga aggcgccgac	660
ggagtgggta gttcctcggg aaattggcat tgcgattcca catggctggg cgacagagtc	720
atcaccacca gcacccgaac ctggggccctg cccacctaca acaaccacct ctacaagcaa	780
atctccaacg ggacatcggg aggagccacc aacgacaaca cctacttcgg ctacagcacc	840
ccctgggggt attttgactt taacagattc cactgccact tttcaccacg tgactggcag	900
cgactcatca acaacaactg gggattccgg cccaagagac tcagcttcaa gctcttcaac	960
atccagggtca aggagggtcac gcagaatgaa ggcaccaaga ccatcgccaa taacctcacc	1020

agcaccatcc aggtgtttac ggactcggag taccagctgc cgtacgttct cggctctgcc	1080
caccaggggt gcctgcctcc gttcccggcg gacgtgttca tgattcccca gtacggctac	1140
ctaactca acaacggtag tcaggccgtg ggacgctcct ctttctactg cctggaatac	1200
tttccttcgc agatgctgag aaccggcaac aacttccagt ttacttacac cttcgaggac	1260
gtgcctttcc acagcagcta cgcacacagc cagagcttgg accggctgat gaatcctctg	1320
attgaccagt acctgtacta cttgtctcgg actcaaaca caggaggcac ggcaaatacg	1380
cagactctgg gcttcagcca aggtgggcct aatacaatgg ccaatcaggc aaagaactgg	1440
ctgccaggac cctgttaccg ccaacaacgc gtctcaacga caaccgggca aaacaacaat	1500
agcaactttg cctggactgc tgggacaaaa taccatctga atggaagaaa ttcattggct	1560
aatcctggca tcgctatggc aacacacaaa gacgacgagg agcggttttt tcccagtaac	1620
gggatcctga tttttggcaa acaaaatgct gccagagaca atgcggatta cagcgatgtc	1680
atgctcacca gcgaggaaga aatcaaaacc actaacctg tggctacaga ggaatacgg	1740
atcgtggcag ataacttgca gcagcaaaac acggctcctc aaattggaac tgtcaacagc	1800
cagggggcct taccgggtat ggtctggcag aaccgggacg tgtacctgca ggggtccatc	1860
tgggccaaga ttcctcacac ggacggcaac ttccaccgt ctccgctgat gggcggcttt	1920
ggcctgaaac atcctccgcc tcagatcctg atcaagaaca cgcctgtacc tgcggatcct	1980
ccgaccacct tcaaccagtc aaagctgaac tctttcatca cgcaatacag caccggacag	2040
gtcagcgtgg aaattgaatg ggagctgcag aaggaaaaca gcaagcgtg gaaccccgag	2100
atccagtaca cctccaacta ctacaaatct acaagtgtgg actttgctgt taatacagaa	2160
ggcgtgtact ctgaaccccg ccccatgtgc acccgttacc tcacccgtaa tctg	2214

<210> 23

<211> 165

<212> DNA

<213> adeno-associated virus 2

<400> 23

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tcacgtgagt gttttgcgac attttgcgac accatgtggt ctcgtgggg gggggggccc	120
gagtgagcac gcagggtctc cattttgaag cgggaggttt gaacg	165

<210> 24
 <211> 1866
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence containing Rep region of serotype 2 AAV,
 synthetic sequence

<400> 24	
acgccggggt tttagagat tgtgattaag gtccccagcg accttgacga gcatctgccc	60
ggcatttctg acagctttgt gaactgggtg gccgagaagg aatgggagtt gccgccagat	120
tctgacatgg atctgaatct gattgagcag gcaccctga ccgtggccga gaagctgcag	180
cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc cggaggccct tttctttgtg	240
caatttgaga agggagagag ctacttccac atgcacgtgc tcgtggaaac caccggggtg	300
aaatccatgg ttttgggacg tttcctgagt cagattcgcg aaaaactgat tcagagaatt	360
taccgcggga tcgagccgac ttgccaac tggttcgcgg tcacaaagac cagaaatggc	420
gccggaggcg ggaacaaggt ggtggatgag tgctacatcc ccaattactt gctcccaaaa	480
accagcctg agctccagtg ggcgtggact aatatggaac agtatttaag cgctgtttg	540
aatctcacgg agcgtaaacg gttggtggcg cagcatctga cgcacgtgtc gcagacgcag	600
gagcagaaca aagagaatca gaatcccaat tctgatgcgc cggatgatcag atcaaaaact	660
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cagtggatcc aggaggacca ggcctcatac atctccttca atgcggcctc caactcgcg	780
tcccaaatca aggctgcctt ggacaatgcg ggaaagatta tgagcctgac taaaaccgcc	840
cccgactacc tgggtggcca gcagcccgtg gaggacattt ccagcaatcg gatttataaa	900
attttgaac taaacgggta cgatcccaa tatgcggctt ccgtctttct gggatgggcc	960
acgaaaaagt tcggcaagag gaacaccatc tggctgtttg ggcctgcaac taccgggaag	1020

accaacatcg cggaggccat agcccacact gtgcccttct acgggtgcgt aaactggacc	1080
aatgagaact ttcccttcaa cgactgtgtc gacaagatgg tgatctggtg ggaggagggg	1140
aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc tcggaggaag caaggtgcgc	1200
gtggaccaga aatgcaagtc ctcggcccag atagaccga cttccgtgat cgtcacctcc	1260
aacaccaaca tgtgcgccgt gattgacggg aactcaacga cttcgaaca ccagcagccg	1320
ttgcaagacc ggatgttcaa atttgaactc acccgccgtc tggatcatga ctttgggaag	1380
gtcaccaagc aggaagtcaa agactttttc cgggtgggcaa aggatcacgt ggttgaggtg	1440
gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa gacccgcccc cagtgcgca	1500
gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc agccatcgac gtcagacgcg	1560
gaagcttcga tcaactacgc agacaggtac caaaacaaat gttctcgtca cgtgggcatg	1620
aatctgatgc tgtttccctg cagacaatgc gagagaatga atcagaattc aaatatctgc	1680
ttcactcacg gacagaaaaga ctgtttagag tgctttcccg tgtcagaatc tcaaccggtt	1740
tctgtcgtca aaaaggcgta tcagaaactg tgctacattc atcatatcat gggaaagggtg	1800
ccagacgctt gcactgcctg cgatctggtc aatgtggatt tggatgactg catctttgaa	1860
caataa	1866

<210> 25
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of primer SI-1, synthetic sequence

<400> 25	
gccagccatc tgttgt	16

<210> 26
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of primer SI-2, synthetic sequence

 <400> 26
 ggagtggcac cttcca 16

 <210> 27
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Nucleic acid sequence of probe SI-1, synthetic sequence

 <400> 27
 tccccgtgc cttccttgac c 21

 <210> 28
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Nucleic acid sequence of primer SI-3, synthetic sequence

 <400> 28
 ggaacccta gtgatggagt t 21

 <210> 29
 <211> 16
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Nucleic acid sequence of primer SI-4, synthetic sequence

 <400> 29
 cggcctcagt gagcga 16

 <210> 30
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Nucleic acid sequence of probe SI-2, synthetic sequence

<400> 30

cactccctct ctgcgcgctc g

21

<210> 31

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of CDR1 in the light chain of anti-hTfR antibody 1

<400> 31

Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
1 5 10

<210> 32

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of CDR1 in the light chain of anti-hTfR antibody 2

<400> 32

Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His
1 5 10 15

<210> 33

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acid sequence of CDR2 in the light chain of anti-hTfR antibody 1

<400> 33

Lys Val Ser Asn Arg Phe
1 5

<210> 34
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR2 in the light chain of anti-hTfR
antibody 2

<400> 34

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 35
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR3 in the light chain of anti-hTfR
antibody 3

<400> 35

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 36
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR1 in the heavy chain of anti-hTfR
antibody 1

<400> 36

Asn Tyr Trp Leu Gly
1 5

<210> 37
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR1 in the heavy chain of anti-hTfR
antibody 2

<400> 37

Gly Tyr Ser Phe Met Asn Tyr Trp
1 5

<210> 38
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR2 in the heavy chain of anti-hTfR
antibody 1

<400> 38

Ile Tyr Pro Gly Gly Asp Tyr Pro
1 5

<210> 39
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR2 in the heavy chain of anti-hTfR
antibody 2

<400> 39

Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe Lys
1 5 10 15

Val

<210> 40
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR3 in the heavy chain of anti-hTfR antibody 1

<400> 40

Ser Gly Asn Tyr Asp Glu Val Ala Tyr
1 5

<210> 41
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of CDR3 in the heavy chain of anti-hTfR antibody 2

<400> 41

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr
1 5 10

<210> 42
<211> 766
<212> PRT
<213> Artificial Sequence

<220>
<223> An example of amino acid sequence of a conjugate of human I2S and the Fab region of the heavy chain of an anti-hTfR antibody

<400> 42

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Ser Glu Thr Gln Ala Asn Ser Thr Thr Asp Ala Leu Asn Val Leu
245 250 255

Leu Ile Ile Val Asp Asp Leu Arg Pro Ser Leu Gly Cys Tyr Gly Asp
260 265 270

Lys Leu Val Arg Ser Pro Asn Ile Asp Gln Leu Ala Ser His Ser Leu
275 280 285

Leu Phe Gln Asn Ala Phe Ala Gln Gln Ala Val Cys Ala Pro Ser Arg
290 295 300

Val Ser Phe Leu Thr Gly Arg Arg Pro Asp Thr Thr Arg Leu Tyr Asp
305 310 315 320

Phe Asn Ser Tyr Trp Arg Val His Ala Gly Asn Phe Ser Thr Ile Pro
325 330 335

Gln Tyr Phe Lys Glu Asn Gly Tyr Val Thr Met Ser Val Gly Lys Val
340 345 350

Phe His Pro Gly Ile Ser Ser Asn His Thr Asp Asp Ser Pro Tyr Ser
355 360 365

Trp Ser Phe Pro Pro Tyr His Pro Ser Ser Glu Lys Tyr Glu Asn Thr
370 375 380

Lys Thr Cys Arg Gly Pro Asp Gly Glu Leu His Ala Asn Leu Leu Cys
385 390 395 400

Pro Val Asp Val Leu Asp Val Pro Glu Gly Thr Leu Pro Asp Lys Gln
405 410 415

Ser Thr Glu Gln Ala Ile Gln Leu Leu Glu Lys Met Lys Thr Ser Ala
420 425 430

Ser Pro Phe Phe Leu Ala Val Gly Tyr His Lys Pro His Ile Pro Phe
435 440 445

Arg Tyr Pro Lys Glu Phe Gln Lys Leu Tyr Pro Leu Glu Asn Ile Thr
450 455 460

Leu Ala Pro Asp Pro Glu Val Pro Asp Gly Leu Pro Pro Val Ala Tyr
465 470 475 480

Asn Pro Trp Met Asp Ile Arg Gln Arg Glu Asp Val Gln Ala Leu Asn
485 490 495

Ile Ser Val Pro Tyr Gly Pro Ile Pro Val Asp Phe Gln Arg Lys Ile
500 505 510

Arg Gln Ser Tyr Phe Ala Ser Val Ser Tyr Leu Asp Thr Gln Val Gly
515 520 525

Arg Leu Leu Ser Ala Leu Asp Asp Leu Gln Leu Ala Asn Ser Thr Ile
530 535 540

Ile Ala Phe Thr Ser Asp His Gly Trp Ala Leu Gly Glu His Gly Glu
545 550 555 560

Trp Ala Lys Tyr Ser Asn Phe Asp Val Ala Thr His Val Pro Leu Ile
565 570 575

Phe Tyr Val Pro Gly Arg Thr Ala Ser Leu Pro Glu Ala Gly Glu Lys
580 585 590

Leu Phe Pro Tyr Leu Asp Pro Phe Asp Ser Ala Ser Gln Leu Met Glu
595 600 605

Pro Gly Arg Gln Ser Met Asp Leu Val Glu Leu Val Ser Leu Phe Pro
610 615 620

Thr Leu Ala Gly Leu Ala Gly Leu Gln Val Pro Pro Arg Cys Pro Val

625 630 635 640

His Phe Arg Phe Arg Asp Leu Glu Glu Asp Pro Tyr Leu Pro Gly Asn
660 665 670

Pro Gln Trp Asn Ser Asp Lys Pro Ser Leu Lys Asp Ile Lys Ile Met
690 695 700

Phe Asn Pro Asp Glu Phe Leu Ala Asn Phe Ser Asp Ile His Ala Gly
725 730 735

Asn Asp Ser Gln Gly Gly Asp Leu Phe Gln Leu Leu Met Pro
755 760 765

<220>
<223> A preferable example of nucleic acid sequence of the first Long Terminal Repeat (first LTR) , synthetic sequence

tgaataccaa acaggatatc tgtggtaagc ggttcctgcc ccggctcagg gccaagaaca	180
gatgagacag ctgagtgatg ggccaaacag gatatctgtg gtaagcagtt cctgccccgg	240
ctcggggcca agaacagatg gtccccagat gcgggtccagc cctcagcagt ttctagttaa	300
tcatcagatg tttccagggt gccccaaagga cctgaaaatg accctgtacc ttatttgaac	360
taaccaatca gttcgcttct cgcttctgtt cgcgcgcttc cgctctccga gctcaataaa	420
agagcccaca acccctcact cggcgcgcca gtcttccgat agactgcgtc gcccgggtac	480
ccgtattccc aataaagcct cttgctgttt gcatccgaat cgtgggtctcg ctgttccttg	540
ggagggtctc ctctgagtga ttgactaccc acgacggggg tctttcatt	589

<210> 44
 <211> 594
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A preferable example of nucleic acid sequence of the second Long Terminal Repeat (second LTR) , synthetic sequence

<400> 44	
aatgaaagac ccacactgta ggtttggcaa gctagcttaa gtaacgcat tttgcaaggc	60
atggaaaaat acataactga gaatagagaa gttcagatca aggtcaggaa cagatggaac	120
agctgaatat gggccaaaca ggatatctgt ggtaagcagt tcctgccccg gtcaggggcc	180
aagaacagat ggaacagctg aatatgggcc aaacaggata tctgtggtaa gcagttcctg	240
ccccggctca gggccaagaa cagatggtcc ccagatgcgg tccagccctc agcagtttct	300
agagaaccat cagatgtttc cagggtgccc caaggacctg aaatgaccct gtgccttatt	360
tgaactaacc aatcagttcg cttctcgctt ctgttcgcg cttctgctc cccgagctca	420
ataaaagagc ccacaacccc tctctgggg cgccagtcct ccgattgact gagtcgccccg	480
ggtaaccgtg tatccaataa accctcttgc agttgcatcc gacttgtggc ctcgctgttc	540
cttgggaggg tctcctctga gtgattgact acccgtcagc gggggctttt catt	594

<210> 45

<211> 52
 <212> DNA
 <213> Sendai virus

<400> 45
 accaaacaag agaagaaact tgtttggaat atataatgaa gtttagacagg at 52

<210> 46
 <211> 54
 <212> DNA
 <213> Sendai virus

<400> 46
 acaaggagac aagaaaatth gaaagaataa atatctctta aactcttgct tggt 54

<210> 47
 <211> 4578
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid sequence of the DNA fragment synthesized for
 construction of pAAV-mMAP-Fab-hGLB1 vector, synthetic sequence

<400> 47
 atcgatatca agcttagatc attttgatgg cagagttcag tttaccgggt cacattgtac 60
 ctgggaagat tcaaggatth atggaaaaag tcaacaacag gagtcagagc agccggaaaa 120
 gcatggactc tgtacttagg actgcgctth gagcaatggc acagcaagct ataaccctgt 180
 ttgcagtcag cacacaaact gtggttcaaa gctccactth atctcttctt gtggaattca 240
 gatatcagat cagttttgct caaatgggag acaaagagat taagctctta tgtaaaatth 300
 gctgttttac ataactthaa tgaatggaca aagtcttggt catgggggtg ggggtggggt 360
 tagaggggaa cagctccaga tggcaaakat acgcaaggga tttagtcaaa caactttttg 420
 gcaaagatgg tatgattttg taatggggta ggaaccaatg aaatgagagg taagtatggt 480
 taataatcta cagttattgg ttaaagaagt atattagagc gagtctttct gcacacagat 540
 caccttccta tcaacccac tagcctctgg caaaggtagc agtgtacagg gagtcgctgc 600
 gttgccttcg ccccggtgccc cgctccgagc cgctccgagc cggccgcccc ggctctgact 660

gaccgcgtta ctcccacagg tgagcgggcg ggacggccct tctcctccgg gctgtaatta	720
gcaagaggta agggtttaag ggatggttgg ttggtggggg attaattgttt aattacctgg	780
agcacctgcc tgaaatcact ttttttcagg ttggacgcgt cgccaccatg ggttggagcc	840
tcatcttgct cttccttgtc gctgttgcta cgcgagtcgg cagcgagggtg caactagtgc	900
agtctggagc agagggtgaaa aagcccgggg agtctctgaa gatttcctgt aagggttctg	960
gatacagctt tatgaactac tggctgggat ggggtgcgcca gatgcccggg aaaggcctgg	1020
agtggatggg ggacatctac cccggcggag actaccctac atacagcgag aagttcaagg	1080
tccaggtcac catctcagcc gacaagtcca tcagcaccgc ctacctgcag ttgagcagcc	1140
tgaaggcctc ggacaccgcc atgtattact gtgcgagatc aggcaattac gacgaagtgg	1200
cctactggggg ccaaggaacc ctggtcaccg tctcctcagc tagcaccaag ggcccatcgg	1260
tcttccccct ggcaccctcc tccaagagca cctctggggg cacagcggcc ctgggctgcc	1320
tggtcaagga ctacttcccc gaaccgggtga cgggtgtcgtg gaactcaggc gccctgacca	1380
gcggcgtgca caccttcccc gctgtcctac agtcctcagg actctactcc ctcagcagcg	1440
tggtgaccgt gccctccagc agcttgggca cccagacctt catctgcaac gtgaatcaca	1500
agcccagcaa caccaagggtg gacaagaaag ttgagccgaa gagctgtgat aagacgcata	1560
cgggtggcgg agggctctgga ggtggcggat caggcggagg tggatctcag aggatgttcg	1620
aaattgatta ctcccgggat agcttcctca aagacggcca gccttttagg tacatctccg	1680
gctccattca ctattcccgg gtgcctcgtt ttacttgga agaccggctg ctgaagatga	1740
agatggccgg actgaacgct atccagacct acgtcccttg gaactttcat ggccttggc	1800
ccggccagta ccaatttagc gaggaccacg acgtcgagta ctttttacgg ctggcccacg	1860
aactcggact cctcgtgatt ctgaggcccc gccctacat ttgcgccgag tgggagatgg	1920
gaggtttacc cgcttggctg ctggagaagg agtccatctt attacggagc agcgatcccc	1980
attatttagc cgccgtggac aaatggctgg gagttttact cccaagatg aaacctttac	2040
tgtaccagaa tggcggcccc gttatcaccg tccaagttga gaatgagtat ggctcctatt	2100
tcgcttgcca cttcgactat ttacggtttt tacagaagag gtttcgtcac cacctcggag	2160

acgatgtcgt cctcttcacc accgatggag ccataagac ctttttaaag tgtggcgccc	2220
tccaagggtt atataccacc gtggatttcg gactggtag caacatcaca gatgcctttc	2280
tctcccagcg gaagtgcgaa cctaagggcc ctttaataca ttccgagttc tacaccggct	2340
ggctcgacca ctggggccag cctcactcca ccatcaagac agaagccgtg gccagctctt	2400
tatacgacat cctcgctcgg ggcgctccg tcaatttata catgtttatc ggcggcacca	2460
acttcgccta ttggaacggc gctaactccc cctacgccgc tcagcccaca agctatgact	2520
atgatgcccc tctgtccgaa gccggagatt taaccgagaa gtacttcgcc ctccggaaca	2580
tcattcagaa gttcgagaag gtgcccagg gacctatccc tcccagcacc cccaagttcg	2640
cttacggaaa agtcacccctc gaaaaactga agaccgtggg cgccgcttta gatattctgt	2700
gccccagcgg ccctattaag tctttatacc ccctcacctt tattcaagtt aagcagcatt	2760
acggctttgt tttataccgg accactttac cccaagattg tagcaacccc gtcctctga	2820
gcagcccttt aaacggcgct catgatcggg cttatgtggc tgtcgacggc attccccaag	2880
gtgtgctcga acggaacaac gtgatcactt taaatatcac cggcaaagct ggcgctacac	2940
tggatctgct ggtcgaaaac atgggcccggg tgaactacgg cgcctacatt aacgatttca	3000
agggtttagt gtccaattta aactcagct ccaacattct caccgactgg accatcttcc	3060
ctttagacac cgaggatgct gtgaggagcc atttaggcgg atggggccat cgggacagcg	3120
gacatcacga cgaggcttgg gctcacaata gctccaacta cacactgccc gctttctaca	3180
tgggcaactt cagcatccct agcgggaattc ccgatctgcc tcaagatacc ttcatccaat	3240
tccccggctg gaccaagggc caagtttgga tcaacggctt taatttaggc cggtagtggc	3300
ccgctcgtgg acctcagctg aactgttcg tgcctcaaca cattttaatg acctccgctc	3360
ctaacacaat caccgtgctg gagctggagt gggctccttg tagctccgac gatcccagc	3420
tgtgcgccgt caccttcgtc gatcgtcccg tcacggctc ctccgtgaca tacgaccacc	3480
ccagcaagcc cgttgagaag cggctgatgc ctctcctcc tcagaagaac aaggactctt	3540
ggctggacca cgtgggaagc ggagctacta acttcagcct gctgaagcag gctggagacg	3600

tggaggagaa ccctggacct atgggctgga gctggattct gctgttcctc ctgagcgtga	3660
cagcaggagt gcacagcgac atcgtgatga cccagactcc cctgagcctg agcgtgacac	3720
ctggccagcc tgccagcatc agctgcagaa gctctcagag cctgggtgcac agcaacggca	3780
acacctacct gcactggtat ctgcagaagc ccggccagag ccctcagctg ctgatctaca	3840
aggtgtccaa cagattcagc ggcgtgcccc acagattctc cggcagcggc tctggcaccg	3900
acttcaccct gaagatttcc agagtggaag ccgaggacgt gggcgtgtac tactgcagcc	3960
agagcaccca cgtgccctgg acattcggcc agggcaccaa ggtggaaatc aagagaaccg	4020
tggccgctcc cagcgtgttc atcttccac ctagcgacga gcagctgaag tccggcacag	4080
cctctgtcgt gtgcctgctg aacaacttct acccccgcga ggccaagggtg cagtggaagg	4140
tggacaacgc cctgcagagc ggcaacagcc aggaaagcgt gaccgagcag gactccaagg	4200
acagcaccta cagcctgagc agcacctga ccctgagcaa ggccgactac gagaagcaca	4260
aggtgtacgc ctgcgaagtg acccaccagg gcctgtctag ccccgtagacc aagagcttca	4320
acagaggcga gtgctaataa atttaaatgc ggccgcattt aaatctgtgc cttctagttg	4380
ccagccatct gttgtttgcc cctccccgt gccttccttg accctggaag gtgccactcc	4440
cactgtcctt tcctaataaa atgaggaaat tgcacgcacat tgtctgagta ggtgtcattc	4500
tattctgggg ggtgggggtgg ggcaggacag caagggggag gattgggaag acaatagcag	4560
gcatgctggg gaagatct	4578

<210> 48

<211> 890

<212> PRT

<213> Artificial Sequence

<220>

<223> An example of amino acid sequence of a conjugate of human
fA-galactosidase and the Fab region of the heavy chain of an
anti-hTfR antibody

<400> 48

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1				5					10					15	

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Met Asn Tyr
20 25 30

Trp Leu Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Asp Ile Tyr Pro Gly Gly Asp Tyr Pro Thr Tyr Ser Glu Lys Phe
50 55 60

Lys Val Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Asn Tyr Asp Glu Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
225 230 235 240

Ser Gln Arg Met Phe Glu Ile Asp Tyr Ser Arg Asp Ser Phe Leu Lys
245 250 255

Asp Gly Gln Pro Phe Arg Tyr Ile Ser Gly Ser Ile His Tyr Ser Arg
260 265 270

Val Pro Arg Phe Tyr Trp Lys Asp Arg Leu Leu Lys Met Lys Met Ala
275 280 285

Gly Leu Asn Ala Ile Gln Thr Tyr Val Pro Trp Asn Phe His Glu Pro
290 295 300

Trp Pro Gly Gln Tyr Gln Phe Ser Glu Asp His Asp Val Glu Tyr Phe
305 310 315 320

Leu Arg Leu Ala His Glu Leu Gly Leu Leu Val Ile Leu Arg Pro Gly
325 330 335

Pro Tyr Ile Cys Ala Glu Trp Glu Met Gly Gly Leu Pro Ala Trp Leu
340 345 350

Leu Glu Lys Glu Ser Ile Leu Leu Arg Ser Ser Asp Pro Asp Tyr Leu
355 360 365

Ala Ala Val Asp Lys Trp Leu Gly Val Leu Leu Pro Lys Met Lys Pro
370 375 380

Leu Leu Tyr Gln Asn Gly Gly Pro Val Ile Thr Val Gln Val Glu Asn
385 390 395 400

Glu Tyr Gly Ser Tyr Phe Ala Cys Asp Phe Asp Tyr Leu Arg Phe Leu
405 410 415

Gln Lys Arg Phe Arg His His Leu Gly Asp Asp Val Val Leu Phe Thr
420 425 430

Thr Asp Gly Ala His Lys Thr Phe Leu Lys Cys Gly Ala Leu Gln Gly
435 440 445

Leu Tyr Thr Thr Val Asp Phe Gly Thr Gly Ser Asn Ile Thr Asp Ala
450 455 460

Phe Leu Ser Gln Arg Lys Cys Glu Pro Lys Gly Pro Leu Ile Asn Ser
465 470 475 480

Glu Phe Tyr Thr Gly Trp Leu Asp His Trp Gly Gln Pro His Ser Thr
485 490 495

Ile Lys Thr Glu Ala Val Ala Ser Ser Leu Tyr Asp Ile Leu Ala Arg
500 505 510

Gly Ala Ser Val Asn Leu Tyr Met Phe Ile Gly Gly Thr Asn Phe Ala
515 520 525

Tyr Trp Asn Gly Ala Asn Ser Pro Tyr Ala Ala Gln Pro Thr Ser Tyr
530 535 540

Asp Tyr Asp Ala Pro Leu Ser Glu Ala Gly Asp Leu Thr Glu Lys Tyr
545 550 555 560

Phe Ala Leu Arg Asn Ile Ile Gln Lys Phe Glu Lys Val Pro Glu Gly
565 570 575

Pro Ile Pro Pro Ser Thr Pro Lys Phe Ala Tyr Gly Lys Val Thr Leu
580 585 590

Glu Lys Leu Lys Thr Val Gly Ala Ala Leu Asp Ile Leu Cys Pro Ser

595

600

605

Gly Pro Ile Lys Ser Leu Tyr Pro Leu Thr Phe Ile Gln Val Lys Gln
 610 615 620

His Tyr Gly Phe Val Leu Tyr Arg Thr Thr Leu Pro Gln Asp Cys Ser
 625 630 635 640

Asn Pro Ala Pro Leu Ser Ser Pro Leu Asn Gly Val His Asp Arg Ala
 645 650 655

Tyr Val Ala Val Asp Gly Ile Pro Gln Gly Val Leu Glu Arg Asn Asn
 660 665 670

Val Ile Thr Leu Asn Ile Thr Gly Lys Ala Gly Ala Thr Leu Asp Leu
 675 680 685

Leu Val Glu Asn Met Gly Arg Val Asn Tyr Gly Ala Tyr Ile Asn Asp
 690 695 700

Phe Lys Gly Leu Val Ser Asn Leu Thr Leu Ser Ser Asn Ile Leu Thr
 705 710 715 720

Asp Trp Thr Ile Phe Pro Leu Asp Thr Glu Asp Ala Val Arg Ser His
 725 730 735

Leu Gly Gly Trp Gly His Arg Asp Ser Gly His His Asp Glu Ala Trp
 740 745 750

Ala His Asn Ser Ser Asn Tyr Thr Leu Pro Ala Phe Tyr Met Gly Asn
 755 760 765

Phe Ser Ile Pro Ser Gly Ile Pro Asp Leu Pro Gln Asp Thr Phe Ile
 770 775 780

Gln Phe Pro Gly Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn
 785 790 795 800

Leu Gly Arg Tyr Trp Pro Ala Arg Gly Pro Gln Leu Thr Leu Phe Val
805 810 815

Pro Gln His Ile Leu Met Thr Ser Ala Pro Asn Thr Ile Thr Val Leu
820 825 830

Glu Leu Glu Trp Ala Pro Cys Ser Ser Asp Asp Pro Glu Leu Cys Ala
835 840 845

Val Thr Phe Val Asp Arg Pro Val Ile Gly Ser Ser Val Thr Tyr Asp
850 855 860

His Pro Ser Lys Pro Val Glu Lys Arg Leu Met Pro Pro Pro Pro Gln
865 870 875 880

Lys Asn Lys Asp Ser Trp Leu Asp His Val
885 890

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<211> 66
<212> DNA
<213> Porcine teschovirus-1

<400> 49
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ggacct 66

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<211> 649
<212> PRT
<213> Homo sapiens

<400> 50

Gln Arg Met Phe Glu Ile Asp Tyr Ser Arg Asp Ser Phe Leu Lys Asp
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Gly Gln Pro Phe Arg Tyr Ile Ser Gly Ser Ile His Tyr Ser Arg Val

20

25

30

Pro Arg Phe Tyr Trp Lys Asp Arg Leu Leu Lys Met Lys Met Ala Gly
 35 40 45

Leu Asn Ala Ile Gln Thr Tyr Val Pro Trp Asn Phe His Glu Pro Trp
 50 55 60

Pro Gly Gln Tyr Gln Phe Ser Glu Asp His Asp Val Glu Tyr Phe Leu
 65 70 75 80

Arg Leu Ala His Glu Leu Gly Leu Leu Val Ile Leu Arg Pro Gly Pro
 85 90 95

Tyr Ile Cys Ala Glu Trp Glu Met Gly Gly Leu Pro Ala Trp Leu Leu
 100 105 110

Glu Lys Glu Ser Ile Leu Leu Arg Ser Ser Asp Pro Asp Tyr Leu Ala
 115 120 125

Ala Val Asp Lys Trp Leu Gly Val Leu Leu Pro Lys Met Lys Pro Leu
 130 135 140

Leu Tyr Gln Asn Gly Gly Pro Val Ile Thr Val Gln Val Glu Asn Glu
 145 150 155 160

Tyr Gly Ser Tyr Phe Ala Cys Asp Phe Asp Tyr Leu Arg Phe Leu Gln
 165 170 175

Lys Arg Phe Arg His His Leu Gly Asp Asp Val Val Leu Phe Thr Thr
 180 185 190

Asp Gly Ala His Lys Thr Phe Leu Lys Cys Gly Ala Leu Gln Gly Leu
 195 200 205

Tyr Thr Thr Val Asp Phe Gly Thr Gly Ser Asn Ile Thr Asp Ala Phe
 210 215 220

Leu Ser Gln Arg Lys Cys Glu Pro Lys Gly Pro Leu Ile Asn Ser Glu
225 230 235 240

Phe Tyr Thr Gly Trp Leu Asp His Trp Gly Gln Pro His Ser Thr Ile
245 250 255

Lys Thr Glu Ala Val Ala Ser Ser Leu Tyr Asp Ile Leu Ala Arg Gly
260 265 270

Ala Ser Val Asn Leu Tyr Met Phe Ile Gly Gly Thr Asn Phe Ala Tyr
275 280 285

Trp Asn Gly Ala Asn Ser Pro Tyr Ala Ala Gln Pro Thr Ser Tyr Asp
290 295 300

Tyr Asp Ala Pro Leu Ser Glu Ala Gly Asp Leu Thr Glu Lys Tyr Phe
305 310 315 320

Ala Leu Arg Asn Ile Ile Gln Lys Phe Glu Lys Val Pro Glu Gly Pro
325 330 335

Ile Pro Pro Ser Thr Pro Lys Phe Ala Tyr Gly Lys Val Thr Leu Glu
340 345 350

Lys Leu Lys Thr Val Gly Ala Ala Leu Asp Ile Leu Cys Pro Ser Gly
355 360 365

Pro Ile Lys Ser Leu Tyr Pro Leu Thr Phe Ile Gln Val Lys Gln His
370 375 380

Tyr Gly Phe Val Leu Tyr Arg Thr Thr Leu Pro Gln Asp Cys Ser Asn
385 390 395 400

Pro Ala Pro Leu Ser Ser Pro Leu Asn Gly Val His Asp Arg Ala Tyr
405 410 415

Val Ala Val Asp Gly Ile Pro Gln Gly Val Leu Glu Arg Asn Asn Val
420 425 430

Ile Thr Leu Asn Ile Thr Gly Lys Ala Gly Ala Thr Leu Asp Leu Leu
435 440 445

Val Glu Asn Met Gly Arg Val Asn Tyr Gly Ala Tyr Ile Asn Asp Phe
450 455 460

Lys Gly Leu Val Ser Asn Leu Thr Leu Ser Ser Asn Ile Leu Thr Asp
465 470 475 480

Trp Thr Ile Phe Pro Leu Asp Thr Glu Asp Ala Val Arg Ser His Leu
485 490 495

Gly Gly Trp Gly His Arg Asp Ser Gly His His Asp Glu Ala Trp Ala
500 505 510

His Asn Ser Ser Asn Tyr Thr Leu Pro Ala Phe Tyr Met Gly Asn Phe
515 520 525

Ser Ile Pro Ser Gly Ile Pro Asp Leu Pro Gln Asp Thr Phe Ile Gln
530 535 540

Phe Pro Gly Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu
545 550 555 560

Gly Arg Tyr Trp Pro Ala Arg Gly Pro Gln Leu Thr Leu Phe Val Pro
565 570 575

Gln His Ile Leu Met Thr Ser Ala Pro Asn Thr Ile Thr Val Leu Glu
580 585 590

Leu Glu Trp Ala Pro Cys Ser Ser Asp Asp Pro Glu Leu Cys Ala Val
595 600 605

Thr Phe Val Asp Arg Pro Val Ile Gly Ser Ser Val Thr Tyr Asp His
610 615 620

Pro Ser Lys Pro Val Glu Lys Arg Leu Met Pro Pro Pro Pro Gln Lys
625 630 635 640

Asn Lys Asp Ser Trp Leu Asp His Val
645